CLAIMS

1. A method for combinatorial consensus mutagenesis comprising the steps:

a) identifying a starting gene of interest;

b) identifying at least two homologs of said starting gene of interest;

c) generating a multiple sequence alignment of said at least two homologs of said starting gene of interest, and said starting gene of interest;

d) using said multiple sequence alignment to identify consensus mutations and produce a combinatorial consensus library; and

e) screening said combinatorial consensus library to identify at least one initial hit.

2. The method of Claim 1, further comprising the steps:

f) sequencing said at least one initial hit to provide at least one sequenced initial hit; and

g) identifying improving mutations in said at least one sequenced initial hit.

3. The method of Claim 2, further comprising the steps:

h) using said sequenced initial hits to generate an enhanced combinatorial consensus library; and

i) screening said enhanced combinatorial consensus library to identify at least one improved hit.

3. 4. The method of Claim 3, further comprising the step of sequencing said improved hits.

5. The method of Claim 3, wherein said improved hits are stabilized variants of said starting gene.

6. The method of Claim 3, wherein said improved hits comprise performance-enhancing mutations.

7. The method of Claim 1, wherein said screening comprises determining the stability of said initial hit in at least one assay selected from the group consisting of protease resistance assays, thermostability assays, denaturation assays, and functional assays.

8. The method of Claim 1, further comprising the step of analyzing the correlation between sequence and stability of said at least two initial hits.

9. The method of Claim 3, further comprising the step of analyzing the correlation between sequence and stability of said at least two sequenced improved hits.

10. The method of Claim 1, wherein said multiple sequence alignment identifies amino acids that occur frequently in said homologs but are not part of a consensus sequence.

11. The method of Claim 2, wherein said steps are repeated at least once.

12. The method of Claim 3, wherein said steps are repeated at least once.

13. A sequence improved hit produced according to the method of Claim 3.

14. A sequence improved hit produced according to the method of Claim 2.

15. A combinatorial consensus mutagenesis library produced according to the method of Claim 1.

16. A stabilized variant of beta-lactamase, wherein said stabilized variant comprises at least one amino acid change selected from the group consisting of V11I, V251I, R91K, Q95E, A153S, N232R, S247T, V293L, V294I, T342K, I262V, and V284I.

17. A stabilized variant of carcinoembryonic antigen binder, wherein said stabilized variant comprises at least one amino acid change selected from the group consisting of K3Q, L37V, E42G, E136Q, M146V, F170Y, A194D, and A234G.

18. A stabilized single chain fragment variable region (scFV), wherein said stabilized scFV variant comprises at least one amino acid change selected from the group consisting of K3Q, L37V, E42G, E136Q, M146V, F170Y, A194D, and A234G.